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Sequence Listing was accepted.
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217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=3; day=3; hr=9; min=6; sec=23; ms=273; ]
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Error code      Error Description

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      Diamant, Sophie

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      PREVENTING AND TREATING DISEASES AND DISORDERS ASSOCIATED WITH
      AMYLOID FIBRIL FORMATION

<130> 28870

<140> 10585695
<141> 2009-02-11

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Ser Lys Lys Glu Ser Cys Val Gly Leu
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<213> Homo sapiens

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Leu Leu Leu Cys Met Leu Ile Gly Lys Ser His Thr Glu Asp Asp Ile
            20                  25                  30


Ile Ile Ala Thr Lys Asn Gly Lys Val Arg Gly Met Asn Leu Thr Val
        35                  40                  45

Phe Gly Gly Thr Val Thr Ala Phe Leu Gly Ile Pro Tyr Ala Gln Pro
    50                      55                  60

Pro Leu Gly Arg Leu Arg Phe Lys Lys Pro Gln Ser Leu Thr Lys Trp
65                      70                  75                  80

Ser Asp Ile Trp Asn Ala Thr Lys Tyr Ala Asn Ser Cys Cys Gln Asn
                85                  90                  95

Ile Asp Gln Ser Phe Pro Gly Phe His Gly Ser Glu Met Trp Asn Pro
            100                 105                 110

Asn Thr Asp Leu Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ile Pro
        115                 120                 125

Ala Pro Lys Pro Lys Asn Ala Thr Val Leu Ile Trp Ile Tyr Gly Gly
    130                 135                 140

Gly Phe Gln Thr Gly Thr Ser Ser Leu His Val Tyr Asp Gly Lys Phe
145                 150                 155                 160

Leu Ala Arg Val Glu Arg Val Ile Val Val Ser Met Asn Tyr Arg Val
                165                 170                 175

Gly Ala Leu Gly Phe Leu Ala Leu Pro Gly Asn Pro Glu Ala Pro Gly
            180                 185                 190

Asn Met Gly Leu Phe Asp Gln Gln Leu Ala Leu Gln Trp Val Gln Lys
        195                 200                 205

Asn Ile Ala Ala Phe Gly Gly Asn Pro Lys Ser Val Thr Leu Phe Gly
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Glu Ser Ala Gly Ala Ala Ser Val Ser Leu His Leu Leu Ser Pro Gly
225                 230                 235                 240

Ser His Ser Leu Phe Thr Arg Ala Ile Leu Gln Ser Gly Ser Phe Asn
                245                 250                 255

Ala Pro Trp Ala Val Thr Ser Leu Tyr Glu Ala Arg Asn Arg Thr Leu
            260                 265                 270

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Asn Leu Ala Lys Leu Thr Gly Cys Ser Arg Glu Asn Glu Thr Glu Ile
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Ile Lys Cys Leu Arg Asn Lys Asp Pro Gln Glu Ile Leu Leu Asn Glu
        290                 295                 300

Ala Phe Val Val Pro Tyr Gly Thr Pro Leu Ser Val Asn Phe Gly Pro
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Thr Val Asp Gly Asp Phe Leu Thr Asp Met Pro Asp Ile Leu Leu Glu
                325                 330                 335

Leu Gly Gln Phe Lys Lys Thr Gln Ile Leu Val Gly Val Asn Lys Asp
                340                 345                 350

Glu Gly Thr Ala Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp
        355                 360                 365

Asn Asn Ser Ile Ile Thr Arg Lys Glu Phe Gln Glu Gly Leu Lys Ile
        370                 375                 380

Phe Phe Pro Gly Val Ser Glu Phe Gly Lys Glu Ser Ile Leu Phe His
385                 390                 395                 400

Tyr Thr Asp Trp Val Asp Asp Gln Arg Pro Glu Asn Tyr Arg Glu Ala
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Leu Gly Asp Val Val Gly Asp Tyr Asn Phe Ile Cys Pro Ala Leu Glu
                420                 425                 430

Phe Thr Lys Lys Phe Ser Glu Trp Gly Asn Asn Ala Phe Phe Tyr Tyr
        435                 440                 445

Phe Glu His Arg Ser Ser Lys Leu Pro Trp Pro Glu Trp Met Gly Val
        450                 455                 460

Met His Gly Tyr Glu Ile Glu Phe Val Phe Gly Leu Pro Leu Glu Arg
465                 470                 475                 480

Arg Asp Asn Tyr Thr Lys Ala Glu Glu Ile Leu Ser Arg Ser Ile Val
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Lys Arg Trp Ala Asn Phe Ala Lys Tyr Gly Asn Pro Asn Glu Thr Gln
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Asn Asn Ser Thr Ser Trp Pro Val Phe Lys Ser Thr Glu Gln Lys Tyr
              515                 520                 525


Leu Thr Leu Asn Thr Glu Ser Thr Arg Ile Met Thr Lys Leu Arg Ala
        530                 535                 540


Gln Gln Cys Arg Phe Trp Thr Ser Phe Phe Pro Lys Val Leu Glu Met
545                 550                 555                 560


Thr Gly Asn Ile Asp Glu Ala Glu Trp Glu Trp Lys Ala Gly Phe His
              565                 570                 575


Arg Trp Asn Asn Tyr Met Met Asp Trp Lys Asn Gln Phe Asn Asp Tyr
              580                 585                 590


Thr Ser Lys Lys Glu Ser Cys Val Gly Leu
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<223>   ASP23 Synthetic peptide

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Asp Glu Ala Glu Arg Gln Trp Lys Ala Glu Phe His Arg Trp Ser Ser
              20                  25                  30


Tyr Met Val His Trp Lys Asn Gln Phe Asp His Tyr Ser Lys Gln Asp
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Arg Cys Ser Asp Leu
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Trp Ser Ser Tyr Met Val His Trp Lys Asn Gln Phe Asp His Tyr Ser
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Lys Gln Asp Arg Cys Ser Asp Leu
        35                  40


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<213> Artificial sequence

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<223> ASP63 Synthetic peptide

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Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Asp Thr Leu Asp Glu
            20                  25                  30


Ala Glu Arg Gln Trp Lys Ala Glu Phe His Arg Trp Ser Ser Tyr Met
        35                  40                  45


Val His Trp Lys Asn Gln Phe Asp His Tyr Ser Lys Gln Asp Arg
    50                  55                  60


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<213> Homo sapiens

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Met Arg Pro Pro Gln Cys Leu Leu His Thr Pro Ser Leu Ala Ser Pro
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Leu Leu Leu Leu Leu Leu Trp Leu Leu Gly Gly Gly Val Gly Ala Glu

Gly Arg Glu Asp Ala Glu Leu Leu Val Thr Val Arg Gly Gly Arg Leu
        35                  40                  45

Arg Gly Ile Arg Leu Lys Thr Pro Gly Gly Pro Val Ser Ala Phe Leu
        50                  55                  60

Gly Ile Pro Phe Ala Glu Pro Pro Met Gly Pro Arg Arg Phe Leu Pro
65                  70                  75                  80

Pro Glu Pro Lys Gln Pro Trp Ser Gly Val Val Asp Ala Thr Thr Phe
                85                  90                  95

Gln Ser Val Cys Tyr Gln Tyr Val Asp Thr Leu Tyr Pro Gly Phe Glu
            100                 105                 110

Gly Thr Glu Met Trp Asn Pro Asn Arg Glu Leu Ser Glu Asp Cys Leu
        115                 120                 125

Tyr Leu Asn Val Trp Thr Pro Tyr Pro Arg Pro Thr Ser Pro Thr Pro
        130                 135                 140

Val Leu Val Trp Ile Tyr Gly Gly Gly Phe Tyr Ser Gly Ala Ser Ser
145                 150                 155                 160

Leu Asp Val Tyr Asp Gly Arg Phe Leu Val Gln Ala Glu Arg Thr Val
            165                 170                 175

Leu Val Ser Met Asn Tyr Arg Val Gly Ala Phe Gly Phe Leu Ala Leu
            180                 185                 190

Pro Gly Ser Arg Glu Ala Pro Gly Asn Val Gly Leu Leu Asp Gln Arg
        195                 200                 205

Leu Ala Leu Gln Trp Val Gln Glu Asn Val Ala Ala Phe Gly Gly Asp
        210                 215                 220

Pro Thr Ser Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Ala Ser Val
225                 230                 235                 240

Gly Met His Leu Leu Ser Pro Pro Ser Arg Gly Leu Phe His Arg Ala
            245                 250                 255

Val Leu Gln Ser Gly Ala Pro Asn Gly Pro Trp Ala Thr Val Gly Met
        260                 265                 270

Gly Glu Ala Arg Arg Arg Ala Thr Gln Leu Ala His Leu Val Gly Cys
        275                 280                 285

Pro Pro Gly Gly Thr Gly Gly Asn Asp Thr Glu Leu Val Ala Cys Leu
    290                 295                 300

Arg Thr Arg Pro Ala Gln Val Leu Val Asn His Glu Trp His Val Leu
305                 310                 315                 320

Pro Gln Glu Ser Val Phe Arg Phe Ser Phe Val Pro Val Val Asp Gly
            325                 330                 335

Asp Phe Leu Ser Asp Thr Pro Glu Ala Leu Ile Asn Ala Gly Asp Phe
        340                 345                 350

His Gly Leu Gln Val Leu Val Gly Val Val Lys Asp Glu Gly Ser Tyr
        355                 360                 365

Phe Leu Val Tyr Gly Ala Pro Gly Phe Ser Lys Asp Asn Glu Ser Leu
    370                 375                 380

Ile Ser Arg Ala Glu Phe Leu Ala Gly Val Arg Val Gly Val Pro Gln
385                 390                 395                 400

Val Ser Asp Leu Ala Ala Glu Ala Val Val Leu His Tyr Thr Asp Trp
            405                 410                 415

Leu His Pro Glu Asp Pro Ala Arg Leu Arg Glu Ala Leu Ser Asp Val
        420                 425                 430

Val Gly Asp His Asn Val Val Cys Pro Val Ala Gln Leu Ala Gly Arg
        435                 440                 445

Leu Ala Ala Gln Gly Ala Arg Val Tyr Ala Tyr Val Phe Glu His Arg
    450                 455                 460

Ala Ser Thr Leu Ser Trp Pro Leu Trp Met Gly Val Pro His Gly Tyr
465                 470                 475                 480

Glu Ile Glu Phe Ile Phe Gly Ile Pro Leu Asp Pro Ser Arg Asn Tyr
                485               490               495


Thr Ala Glu Glu Lys Ile Phe Ala Gln Arg Leu Met Arg Tyr Trp Ala
                500               505               510


Asn Phe Ala Arg Thr Gly Asp Pro Asn Glu Pro Arg Asp Pro Lys Ala
        515               520               525


Pro Gln Trp Pro Pro Tyr Thr Ala Gly Ala Gln Gln Tyr Val Ser Leu
    530               535               540


Asp Leu Arg Pro Leu Glu Val Arg Arg Gly Leu Arg Ala Gln Ala Cys
545               550               555               560


Ala Phe Trp Asn Arg Phe Leu Pro Lys Leu Leu Ser Ala Thr Asp Thr
                565               570               575


Leu Asp Glu Ala Glu Arg Gln Trp Lys Ala Glu Phe His Arg Trp Ser
                580               585               590


Ser Tyr Met Val His Trp Lys Asn Gln Phe Asp His Tyr Ser Lys Gln
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Asp Arg Cys Ser Asp Leu
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tgaagatgac atcataattg caacaaagaa tggaaaagtc agagggatga acttgacagt       300

ttttggtggc acggtaacag cctttcttgg aattccctat gcacagccac ctcttggtag       360

acttcgattc aaaaagccac agtctctgac caagtggtct gatatttgga atgccacaaa       420

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gaacagaacg ttgaacttag ctaaattgac tggttgctct agagagaatg agactgaaat   1020

aatcaagtgt cttagaaata aagatcccca agaaattctt ctgaatgaag catttgttgt   1080

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1               5


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